```
                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:        July 12, 2003, 21:05:24 ; Search time 1445 Seconds
                                          (without alignments)
                                          1008.715 Million cell updates/sec

Title:          US-09-910-757-1
Perfect score:  90
Sequence:       1 gggagacggcggcggtggcg.........cggtgccccgccgcagggtcg 90

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:    32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      EST:*
           1:   em_estba:*
           2:   em_esthum:*
           3:   em_estin:*
           4:   em_estmu:*
           5:   em_estov:*
           6:   em_estpl:*
           7:   em_estro:*
           8:   em_htc:*
           9:   gb_est1:*
          10:   gb_est2:*
          11:   gb_htc:*
          12:   gb_est3:*
          13:   gb_est4:*
          14:   gb_est5:*
          15:   em_estfun:*
          16:   em_estom:*
          17:   gb_gss:*
          18:   em_gss_hum:*
          19:   em_gss_inv:*
          20:   em_gss_pln:*
          21:   em_gss_vrt:*
          22:   em_gss_fun:*
          23:   em_gss_mam:*
          24:   em_gss_mus:*
          25:   em_gss_other:*
          26:   em_gss_pro:*
          27:   em_gss_rod:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	90	100.0	300	9	AU098678	AU098678 AU098678
2	90	100.0	350	12	BE831859	BE831859 RC6-MT006
3	90	100.0	447	14	BM694414	BM694414 UI-E-CII-
4	90	100.0	571	13	BI547746	BI547746 603191906
5	90	100.0	635	13	BI547550	BI547550 603190969
6	90	100.0	653	9	AL042549	AL042549 DKFZp434I

7	90	100.0	657	12	BG722295	BG722295 602693472
8	90	100.0	677	13	BI559391	BI559391 603253071
9	90	100.0	679	13	BI597041	BI597041 603248271
10	90	100.0	685	12	BG719125	BG719125 602699058
11	90	100.0	701	13	BM172428	BM172428 imageqc_4
12	90	100.0	705	12	BI545908	BI545908 603188306
13	90	100.0	715	12	BG709029	BG709029 602675179
14	90	100.0	716	12	BI544366	BI544366 603241762
15	90	100.0	734	12	BG704185	BG704185 602687727
16	90	100.0	776	12	BG764788	BG764788 602736395
17	90	100.0	785	13	BI761515	BI761515 603046658
18	90	100.0	829	13	BI561536	BI561536 603256235
19	90	100.0	867	12	BF315675	BF315675 601899329
20	90	100.0	869	9	AL550975	AL550975 AL550975
21	90	100.0	891	14	BQ897731	BQ897731 AGENCOURT
22	90	100.0	895	12	BF204878	BF204878 601867185
23	90	100.0	900	14	BQ440126	BQ440126 AGENCOURT
24	90	100.0	920	9	AL543516	AL543516 AL543516
25	90	100.0	929	12	BF979775	BF979775 602288671
26	90	100.0	931	14	BQ688437	BQ688437 AGENCOURT
27	90	100.0	944	9	AL550425	AL550425 AL550425
28	90	100.0	969	14	BQ080712	BQ080712 AGENCOURT
29	90	100.0	1031	9	AL533088	AL533088 AL533088
30	90	100.0	1494	14	BQ706464	BQ706464 AGENCOURT
31	88.8	98.7	895	9	AL537562	AL537562 AL537562
32	88.8	98.7	897	9	AL518480	AL518480 AL518480
33	88.4	98.2	641	13	BI545987	BI545987 603188112
34	88.4	98.2	699	9	AU137092	AU137092 AU137092
35	88.4	98.2	821	9	AL557346	AL557346 AL557346
36	88	97.8	612	9	AU128077	AU128077 AU128077
37	88	97.8	911	9	AL532648	AL532648 AL532648
38	87.4	97.1	639	14	BQ807996	BQ807996 NISC_kk12
39	86	95.6	862	12	BE735858	BE735858 601305192
40	85.2	94.9	772	12	BG701016	BG701016 602682011
41	85.2	94.7	1050	14	BQ882754	BQ882754 AGENCOURT
42	79	87.8	712	12	BG720447	BG720447 602691751
43	79	87.8	728	13	BI601746	BI601746 603249996
44	78	86.7	723	12	BE867517	BE867517 601443015
45	77.4	86.0	154	9	AU077057	AU077057 AU077057

                                  ALIGNMENTS

RESULT 1
AU098678
LOCUS   AU098678   300 bp   mRNA   linear   EST 05-APR-2001
DEFINITION AU098678 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            COL09158 similar to Human mRNA for amyloid A4 precursor of
            Alzheimer's disease, mRNA sequence.
ACCESSION   AU098678
VERSION   AU098678.1 GI:13549807
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 300)
AUTHORS   Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
            ,K., Suyama,A. and Sugano,S.
TITLE   In silico mapping of the 5'-ends of human mRNAs using full-length
            enriched and 5'-end enriched cDNA libraries constructed by
            Oligo-capping method
JOURNAL   Unpublished (2001)
COMMENT   Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

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FEATURES             Location/Qualifiers
     source          1..300
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="COL09158"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"

BASE COUNT     50 a        86 c       112 g       52 t
ORIGIN

          Query Match          100.0%;   Score 90;  DB 9;  Length 300;
          Best Local Similarity 100.0%;  Pred. No. 6.2e-13;
          Matches  90;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

     Qy     1 GGGAGACGGCGGCGGTGGCGGCGGCGGCGGCCAGAGCAAGGACGGCGGCGGATCCCACTCGCACA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db    56 GGGAGACGGCGGCGGTGGCGGCGGCGGCGGCCAGAGCAAGGACGGCGGCGGATCCCACTCGCACA 115

     Qy    61 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 90
               ||||||||||||||||||||||||||||||
     Db   116 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 145

RESULT 2
BE831859/c
LOCUS       BE831859              350 bp    mRNA    linear    EST 22-SEP-2000
DEFINITION  RC6-MT0061-310700-021-G04 MT0061 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE831859
VERSION     BE831859.1  GI:1026423
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 350)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
COMMENT     Contact: Simpson A.J.G.
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-st2=RC6-MT0061-310
            700-021-G04&t3-2000-07-31&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 345.

FEATURES             Location/Qualifiers
     source          1..350
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MT0061"
                     /dev_stage="Adult"
                     /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 - Ludwig Institute for Cancer Research) profiles
                     into the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."

BASE COUNT     60 a       114 c       104 g       71 t        1 others
ORIGIN

          Query Match          100.0%;   Score 90;  DB 12;  Length 350;
          Best Local Similarity 100.0%;  Pred. No. 6.4e-13;
          Matches  90;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

     Qy     1 GGGAGACGGCGGCGGTGGCGGCGGCGGCGGCCAGAGCAAGGACGGCGGCGGATCCCACTCGCACA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db   333 GGGAGACGGCGGCGGTGGCGGCGGCGGCGGCCAGAGCAAGGACGGCGGCGGATCCCACTCGCACA 274

     Qy    61 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 90
               ||||||||||||||||||||||||||||||
     Db   273 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 244

RESULT 3
BM694414
LOCUS       BM694414              447 bp    mRNA    linear    EST 28-FEB-2002
DEFINITION  UI-E-CII-afq-d-05-0-UI.r1 UI-E-CII Homo sapiens cDNA clone
            UI-E-CII-afq-d-05-0-UI 5', mRNA sequence.
ACCESSION   BM694414
VERSION     BM694414.1  GI:19007672
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 447)
AUTHORS     Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.

FEATURES             Location/Qualifiers
     source          1..447
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-CII-afq-d-05-0-UI"
                     /clone_lib="UI-E-CII"
                     /tissue_type="RPE and Choroid"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye: Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-CII is a normalized cDNA library containing the
                     following tissue(s): RPE and Choroid. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is ACCTA.
                     This library was created for the program, Gene Discovery
                     in the Visual System, supported by National Eye Institute
                     (NEI)."
```

```
BASE COUNT       99 a      136 c      136 g       76 t
ORIGIN

Query Match          100.0%;  Score 90;  DB 14;  Length 447;
Best Local Similarity 100.0%;  Pred. No. 6.6e-13;
Matches  90;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GGGAGACGGCGGCGGTGCGGCGCGGGCAGAGCAAGGACGCGCGGCGGATCCCACTCGCACA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5 GGGAGACGGCGGCGGTGCGGCGCGGGCAGAGCAAGGACGCGCGGCGGATCCCACTCGCACA 64

Qy   61 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 90
        ||||||||||||||||||||||||||||||
Db   65 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 94

RESULT 4
BI547746
LOCUS       BI547746                    571 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603191906F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5263249 5',
            mRNA sequence.
ACCESSION   BI547746
VERSION     BI547746.1  GI:15435058
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11663 row: 1 column: 02
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1..571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5263249"
                     /clone_lib="NIH_MGC_95"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation). Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      125 a      161 c      181 g      104 t
ORIGIN

Query Match          100.0%;  Score 90;  DB 13;  Length 571;
Best Local Similarity 100.0%;  Pred. No. 6.9e-13;
Matches  90;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GGGAGACGGCGGCGGTGCGGCGCGGGCAGAGCAAGGACGCGCGGCGGATCCCACTCGCACA 60
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Db   61 GGGAGACGGCGGCGGTGCGGCGCGGGCAGAGCAAGGACGCGCGGCGGATCCCACTCGCACA 120

Qy   61 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 90
```

```
Db  121 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 150

RESULT 5
BI547550
LOCUS       BI547550                    635 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603190969F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262424 5',
            mRNA sequence.
ACCESSION   BI547550
VERSION     BI547550.1  GI:15434862
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 635)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11661 row: 1 column: 17
            High quality sequence stop: 634.
FEATURES             Location/Qualifiers
     source          1..635
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5262424"
                     /clone_lib="NIH_MGC_95"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation). Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      147 a      177 c      196 g      115 t
ORIGIN

Query Match          100.0%;  Score 90;  DB 13;  Length 635;
Best Local Similarity 100.0%;  Pred. No. 7.1e-13;
Matches  90;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GGGAGACGGCGGCGGTGCGGCGCGGGCAGAGCAAGGACGCGCGGCGGATCCCACTCGCACA 60
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Db   43 GGGAGACGGCGGCGGTGCGGCGCGGGCAGAGCAAGGACGCGCGGCGGATCCCACTCGCACA 102

Qy   61 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 90
        ||||||||||||||||||||||||||||||
Db  103 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 132

RESULT 6
AL042549
LOCUS       AL042549                    653 bp    mRNA    linear   EST 29-FEB-2000
DEFINITION  DKFZp43412421_r1 434 (synonym: htes3) Homo sapiens cDNA clone
            DKFZp43412421 5', mRNA sequence.
ACCESSION   AL042549
VERSION     AL042549.1  GI:5422004
KEYWORDS    EST.
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SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 653)
AUTHORS   Blum.H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE   EST (Blum, et al.)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Blum H
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by LMU (Ludwig Maximilians University,
            Munich/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            No s1 sequence available.
            This clone (DKFZp43kI2421) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES   Location/Qualifiers
     source   1..653
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp43kI2421"
                     /clone_lib="434 (synonym: htes3)"
                     /tissue_type="testis"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
                     1 others
BASE COUNT   150 a   183 c   198 g   121 t
ORIGIN

Query Match   100.0%; Score 90; DB 9; Length 653;
Best Local Similarity   100.0%; Pred. No. 7.1e-13;
Matches   90; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGAGACGGCGGCGGTGGCGCGGGCAGAGCAAGAGACGCGGCGGGATCCCCACTCGCACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46 GGGAGACGGCGGCGGTGGCGCGGGCAGAGCAAGAGACGCGGCGGGATCCCCACTCGCACA 105

Qy   61 GCAGCGCACTCGGTGCCCCGCCGCAGGGTCG 90
              |||||||||||||||||||||||||||||||
Db   106 GCAGCGCACTCGGTGCCCCGCCGCAGGGTCG 135

RESULT 7
BG722295
LOCUS   BG722295   657 bp   mRNA   linear   EST 08-MAY-2001
DEFINITION 602693472F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4825960 5',
            mRNA sequence.
ACCESSION   BG722295
VERSION   BG722295.1 GI:14001482
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 657)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL).
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov

Plate: LLAM10739 row: o column: 17
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                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.2 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation). Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT   150 a   182 c   203 g   122 t
ORIGIN

Query Match   100.0%; Score 90; DB 12; Length 657;
Best Local Similarity   100.0%; Pred. No. 7.1e-13;
Matches   90; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGAGACGGCGGCGGTGGCGCGGGCAGAGCAAGAGACGCGGCGGGATCCCCACTCGCACA 60
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Db   64 GGGAGACGGCGGCGGTGGCGCGGGCAGAGCAAGAGACGCGGCGGGATCCCCACTCGCACA 123

Qy   61 GCAGCGCACTCGGTGCCCCGCCGCAGGGTCG 90
              |||||||||||||||||||||||||||||||
Db   124 GCAGCGCACTCGGTGCCCCGCCGCAGGGTCG 153

RESULT 8
BI559391
LOCUS   BI559391   677 bp   mRNA   linear   EST 05-SEP-2001
DEFINITION 603253071F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295569 5',
            mRNA sequence.
ACCESSION   BI559391
VERSION   BI559391.1 GI:15446705
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 677)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Clone Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11747 row: n column: 18
            High quality sequence stop: 677.
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                     /lab_host="DH10B"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.2 kb and

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                normalized to ROT 5. This is a primary library enriched
                for full-length clones and constructed using the
                Cap-trapper method (Carninci, in preparation). Library
                constructed by M. Brownstein (NIMH/NHGRI, National
                Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      143 a    199 c    212 g    123 t
ORIGIN

Query Match        100.0%;  Score 90;  DB 13;  Length 677;
Best Local Similarity   100.0%;  Pred. No. 7.2e-13;
Matches   90;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 GGGAGACGGCGCGGCGGTGGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 60
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Db    114 GGGAGACGGCGCGGCGGTGGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 173

Qy     61 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 90
          ||||||||||||||||||||||||||||||
Db    174 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 203

RESULT 9
BI597041
LOCUS       BI597041              679 bp   mRNA      linear   EST 07-SEP-2001
DEFINITION  603248271F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5300177 5',
            mRNA sequence.
ACCESSION   BI597041
VERSION     BI597041.1  GI:15489980
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11759  row: n  column: 18
            High quality sequence stop: 675.
FEATURES             Location/Qualifiers
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                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.3 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation). Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      155 a    186 c    210 g    128 t
ORIGIN

Query Match        100.0%;  Score 90;  DB 13;  Length 679;
Best Local Similarity   100.0%;  Pred. No. 7.2e-13;
Matches   90;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      1 GGGAGACGGCGCGGCGGTGGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 60
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Db     39 GGGAGACGGCGCGGCGGTGGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 98

Qy     61 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 90
          ||||||||||||||||||||||||||||||
Db     99 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 128

RESULT 10
BG719125
LOCUS       BG719125              685 bp   mRNA      linear   EST 08-MAY-2001
DEFINITION  602699058F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831046 5',
            mRNA sequence.
ACCESSION   BG719125
VERSION     BG719125.1  GI:13998312
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 685)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10753  row: c  column: 15
            High quality sequence stop: 684.
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                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.2 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation). Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      160 a    184 c    204 g    137 t
ORIGIN

Query Match        100.0%;  Score 90;  DB 12;  Length 685;
Best Local Similarity   100.0%;  Pred. No. 7.2e-13;
Matches   90;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 GGGAGACGGCGCGGCGGTGGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6 GGGAGACGGCGCGGCGGTGGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 65

Qy     61 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 90
          ||||||||||||||||||||||||||||||
Db     66 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 95

RESULT 11
BM172428
LOCUS       BM172428              701 bp   mRNA      linear   EST 04-DEC-2001
DEFINITION  imageqc_4_2001/smv76bdff41.x1 NIH_MGC_97 Homo sapiens cDNA clone
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ACCESSION   IMAGE:4829092 5', mRNA sequence.
VERSION   BM172428
VERSION   BM172428.1   GI:1731991
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 701)
AUTHORS   Kale,P.I., Harsch,T.J., Folta,P.A., Nelson,D.O., Sanders,C.G. and
            Prange.C.K.
TITLE   The I.M.A.G.E. Consortium quality control effort: clone
            resequencing for verification
JOURNAL   Unpublished (2001)
COMMENT   Contact: Prange CK
            The I.M.A.G.E. Consortium
            Lawrence Livermore National Laboratory
            Livermore, CA, USA
            Email: help@image.llnl.gov
            This read has been produced as part of the I.M.A.G.E. Consortium
            quality control effort. High quality sequence is defined as having
            100 or more base pairs with a phred quality value of 20 or greater,
            where a sliding window of 4 base pairs with a phred quality value
            of 15 or greater marks the beginning and end of the sequence. For
            information on obtaining this clone, please contact
            info@image.llnl.gov.
            Plate: LLAM10748 row: b column: 5
            Seq primer: -21m13
            High quality sequence stop: 701.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4829092"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.2 kb and
                     normalized to ROT 5. This is a primary library enriched.
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation). Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT   151 a   202 c   216 g   128 t   4 others
ORIGIN

Query Match   100.0%; Score 90; DB 13; Length 701;
Best Local Similarity   100.0%; Pred. No. 7.2e-13;
Matches   90; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGAGACGGGCGCGGCGGTGGCGGCCGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   109 GGGAGACGGGCGCGGCGGTGGCGGCCGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 168

Qy   61 GCAGCGCACTCGGTGCCCCGCCGCAGGGTCG 90
          |||||||||||||||||||||||||||||||
Db   169 GCAGCGCACTCGGTGCCCCGCCGCAGGGTCG 198

RESULT 12
BI545908
LOCUS   BI545908   705 bp   mRNA   linear   EST 05-SEP-2001
DEFINITION 603188306F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5259793 5',
            mRNA sequence.
ACCESSION   BI545908
VERSION   BI545908.1   GI:15433220
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 705)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11654 row: 1 column: 02
            High quality sequence stop: 675.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_95"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation). Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT   161 a   191 c   225 g   128 t
ORIGIN

Query Match   100.0%; Score 90; DB 13; Length 705;
Best Local Similarity   100.0%; Pred. No. 7.2e-13;
Matches   90; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGAGACGGGCGCGGCGGTGGCGGCCGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 60
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Db   61 GGGAGACGGGCGCGGCGGTGGCGGCCGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 120

Qy   61 GCAGCGCACTCGGTGCCCCGCCGCAGGGTCG 90
          |||||||||||||||||||||||||||||||
Db   121 GCAGCGCACTCGGTGCCCCGCCGCAGGGTCG 150

RESULT 13
BG709029
LOCUS   BG709029   715 bp   mRNA   linear   EST 07-MAY-2001
DEFINITION 602675179F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4797883 5',
            mRNA sequence.
ACCESSION   BG709029
VERSION   BG709029.1   GI:13986960
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae. Homo.
REFERENCE   1 (bases 1 to 715)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be

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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10684 row: m column: 20
High quality sequence stop: 697.
FEATURES
     source
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              /organism="Homo sapiens"
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              /tissue_type="hypothalamus"
              /lab_host="DH10B"
              /note="Organ: brain; Vector: pBluescriptR (modified
              pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
              ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
              size-selected for average insert size 2.3 kb and
              normalized to ROT 5. This is a primary library enriched
              for full-length clones and constructed using the
              Cap-trapper method (Carninci, in preparation). Library
              constructed by M. Brownstein (NIMH/NHGRI, National
              Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      162 a      193 c      223 g      137 t
ORIGIN

Query Match
Best Local Similarity  100.0%;     Score 90;   DB 12;   Length 715;
Matches 90;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 GGGAGACGGCGGCGGCGGTGGCGGCGGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 60
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Db    60 GGGAGACGGCGGCGGCGGTGGCGGCGGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 119

Qy    61 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 90
         ||||||||||||||||||||||||||||||
Db   120 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 149


RESULT 14
BI544366
LOCUS       BI544366       716 bp    mRNA     linear     EST 05-SEP-2001
DEFINITION  603241762F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5284359 5',
            mRNA sequence.
ACCESSION   BI544366
VERSION     BI544366.1   GI:15431678
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 716)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11718 row: k column: 16
            High quality sequence stop: 699.
FEATURES
     source
              1..716
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="IMAGE:5284359"
              /clone_lib="NIH_MGC_95"
              /tissue_type="hippocampus"
              /lab_host="DH10B"
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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10684 row: m column: 20
Plate: LLAM10724 row: f column: 07
High quality sequence stop: 701.
FEATURES
     source
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              /organism="Homo sapiens"
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              /clone="IMAGE:4819974"
              /clone_lib="NIH_MGC_95"
              /tissue_type="hippocampus"
              /lab_host="DH10B"
              /note="Organ: brain; Vector: pBluescriptR (modified
              pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
              ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
              size-selected for average insert size 2.5 kb and
              normalized to ROT 5. This is a primary library enriched
              for full-length clones and constructed using the
              Cap-trapper method (Carninci, in preparation). Library
              constructed by M. Brownstein (NIMH/NHGRI, National
              Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      165 a      199 c      227 g      143 t
ORIGIN


/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      162 a      193 c      224 g      137 t
ORIGIN

Query Match
Best Local Similarity  100.0%;     Score 90;   DB 13;   Length 716;
Matches 90;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 GGGAGACGGCGGCGGCGGTGGCGGCGGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GGGAGACGGCGGCGGCGGTGGCGGCGGCGGCCAGAGCAAGGACGCGGCGGATCCCACTCGCACA 120

Qy    61 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 90
         ||||||||||||||||||||||||||||||
Db   121 GCAGCGCACTCGGTGCCCCGCGCAGGGTCG 150


RESULT 15
BG704185
LOCUS       BG704185       734 bp    mRNA     linear     EST 07-MAY-2001
DEFINITION  602687727F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4819974 5',
            mRNA sequence.
ACCESSION   BG704185
VERSION     BG704185.1   GI:13977267
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 734)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10724 row: f column: 07
            High quality sequence stop: 701.
FEATURES
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Query Match   100.0%;   Score 90;   DB 12;   Length 734;
Best Local Similarity   100.0%;   Pred. No. 7.3e-13;
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Qy   1 GGGAGACGGCGCGGTGGCGCGGCGCAGAGCAAGGACGCGGCGATCCCACTCGCACA 60
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Db   64 GGGAGACGGCGCGGTGGCGCGGCGCAGAGCAAGGACGCGGCGATCCCACTCGCACA 123

Qy   61 GCAGCGCACTCGGTGCCCCGGCCAGGGTCG 90
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Db   124 GCAGCGCACTCGGTGCCCCGGCCAGGGTCG 153

Search completed: July 12, 2003, 21:58:09
Job time : 1450 secs